SEQUENCE LISTING

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       Jelinek, Laura
       Hirsch, Alec
       DeFilippis, Victor

<120> METHODS OF TREATMENT AND DIAGNOSIS USING MODULATORS OF
       VIRUS-INDUCED CELLULAR GENE SEQUENCES

<130> 899-73077-04

<140> US
<141> 2004-04-15

<150> PCT/US2004/011988
<151> 2004-04-15

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<151> 2003-07-11

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<151> 2003-12-29

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Cys Thr Glu Lys Ile Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser

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Glu His Glu Gln Arg Ala Arg Ala Ser Gly Ala Gly Ala Gly Ala Gly
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Asn Ala His Ala Gly His Ser Gly Leu Leu His Gly Pro Ala Ser Arg
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agc cat cga gcg cga ccc cgc cca gca cga gaa gct cat cgt ccg cat        627
Ser His Arg Ala Arg Pro Arg Pro Ala Arg Glu Ala His Arg Pro His
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Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser Ser Gly Leu Met Asn
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Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys Asp Gly Phe Ser Thr
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Gly Ala Ala Ala Ala Ala Pro Gly Arg Ala Pro Gly Ala His Arg Gln
145                 150                 155                 160

Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg Asn Ala His Ala Gly
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His Ser Gly Leu Leu His Gly Pro Ala Ser Arg Ser His Arg Ala Arg
            180                 185                 190

Pro Arg Pro Ala Arg Glu Ala His Arg Pro His Gln Gly Asn Pro Gly
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Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly Arg Ala His Asp Ala
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Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr Pro Pro Arg Gly Arg
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Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser His Pro Ala Pro Leu
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Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys Ser Ile Pro Leu Ala
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ctgcttctga ctcgattaaa aagggagtga gccataactg gcggctgctc tttcgcca   178

atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag   226
Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu
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            20   25   30

gtc ctg agc act atc tgc ttg gtc aca gta ggg ctc aac ctg ctg gtg   322
Val Leu Ser Thr Ile Cys Leu Val Thr Val Gly Leu Asn Leu Leu Val
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ctg tat gcc gta cgg agt gag cgg aag ctc cac act gtg ggg aac ctg   370
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Tyr Ile Val Ser Leu Ser Val Ala Asp Leu Ile Val Gly Ala Val Val
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atg cct atg aac atc ctc tac ctg ctc atg tcc aag tgg tca ctg ggc   466
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Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr
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gcg tcc att ttc agt gtc ttc atc ctg tgc att gat cgc tac cgc tct   562
Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser
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gtc cag cag ccc ctc agg tac ctt aag tat cgt acc aag acc cga gcc   610
Val Gln Gln Pro Leu Arg Tyr Leu Lys Tyr Arg Thr Lys Thr Arg Ala
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Leu Asp Ile Val His Met Gln Ala Ala Ala Glu Gly Ser Ser Arg Asp
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Tyr Val Ala Val Asn Arg Ser His Gly Gln Leu Lys Thr Asp Glu Gln
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gat tac atc aag ttt act tgg aag agg ctc cgc tcg cat tca aga cag      1378
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tat gta tct ggg ttg cac atg aac cgc gaa agg aag gcc gcc aaa cag      1426
Tyr Val Ser Gly Leu His Met Asn Arg Glu Arg Lys Ala Ala Lys Gln
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aaaaataata aaaataaaag agagagagaa tcagacctgg gtggaactct cctgctcctc    1980

aggaactatg ggagcctcag actcattgta attcaagctt tccgagtcaa gtgattgaca    2040

actgaagaga cacgtggcta gggttccact ggagaattga aaaggactct tgagccctcc    2100

tggaatggag ctgtataact gtgcagagac tttatccatg ccaatagttg ctgtccccctt    2160

ccaggggtca ccttgagagg catgacagct gttccacagg ggctatccct tctcagaaaa    2220

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attctgcctt attatttctt actcaaacat gtttagagtg gatagaaaat tatgcagctt    2340

gcacacccat cgtctttaac cccaaatttc ctttggctat taaaaaagtg gtggcaaaag    2400

gcatcctcaa aagaaagaga aatgaaatat ttttgaatgg ttgcacgtta aaaattaaaa    2460

gaaggaatgg gggcagaatg ccatattttt gagggctgta ctaggtttat ctcatttaag    2520

ccccacaaca ccccacagga gggtaatttt ctaactctag tttgcagagg agcaaattga    2580

ggttcagcaa ggtgagagag gtacccaagg tcacatagct agttatgtga gaaagttaga    2640

gtacagatcc tctggggttt tcagcttatt gtagcatatt ttctccgaaa ggcaaaaatg    2700

tgccctttttg gccgggcatg gtagctcaag cctataatcc cagcatgttg agaggctgag    2760

gtgggcagat catttgaggc caggagttca agaccagtct ggccaatatg gagaaacctt    2820

gtctctacta aaaacacaaa aattatctgg gcatggtggg gcatgcctgt agtcccactt    2880

acttgggagg ccgaggcacg agaatcgctt gaacccggga ggtggaggtt gccgtgagcc    2940
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aagatcacgc cactgcactc cagcctgggc aacagagcaa gactctgtct caaaaaaaaa   3000

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tctgttgtgt ttgtcaaaaa gtcattgtaa tctttcatag ccatacctgg taagcaaaaa   3240

ctagtaaaga cataggaaca tgcagtttta cttggtgttt atgttgcaat ctggttgtga   3300

tttatatttt aaagcttggt gctaaaccac aatatgtata gcacatggag tgcctgtaca   3360

agctgatgtt ttgtattttg tgttcctctt tgcatgatct gtcaaagtga gatattttta   3420

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                                                          Met Glu Asn
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gga tac acc tat gaa gat tat aag aac act gca gaa tgg ctt ctg tct   166
Gly Tyr Thr Tyr Glu Asp Tyr Lys Asn Thr Ala Glu Trp Leu Leu Ser
 5   10   15

cat act aag cac cga cct caa gtt gca ata atc tgt ggt tct gga tta   214
His Thr Lys His Arg Pro Gln Val Ala Ile Ile Cys Gly Ser Gly Leu
20   25   30   35

gga ggt ctg act gat aaa tta act cag gcc cag atc ttt gac tac agt   262
Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe Asp Tyr Ser
                40   45   50

gaa atc ccc aac ttt cct cga agt aca gtg cca ggt cat gct ggc cga   310
Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His Ala Gly Arg
                55   60   65

ctg gtg ttt ggg ttc ctg aat ggc agg gcc tgt gtg atg atg cag ggc   358
Leu Val Phe Gly Phe Leu Asn Gly Arg Ala Cys Val Met Met Gln Gly
            70   75   80

agg ttc cac atg tat gaa ggg tac cca ctc tgg aag gtg aca ttc cca   406

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Arg Phe His Met Tyr Glu Gly Tyr Pro Leu Trp Lys Val Thr Phe Pro
    85                  90              95

gtg agg gtt ttc cac ctt ctg ggt gtg gac acc ctg gta gtc acc aat      454
Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val Val Thr Asn
100              105              110              115

gca gca gga ggg ctg aac ccc aag ttt gag gtt gga gat atc atg ctg      502
Ala Ala Gly Gly Leu Asn Pro Lys Phe Glu Val Gly Asp Ile Met Leu
                120              125              130

atc cgt gac cat atc aac cta cct ggt ttc agt ggt cag aac cct ctc      550
Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln Asn Pro Leu
            135              140              145

aga ggg ccc aat gat gaa agg ttt gga gat cgt ttc cct gcc atg tct      598
Arg Gly Pro Asn Asp Glu Arg Phe Gly Asp Arg Phe Pro Ala Met Ser
        150              155              160

gat gcc tac gac cgg act atg agg cag agg gct ctc agt acc tgg aaa      646
Asp Ala Tyr Asp Arg Thr Met Arg Gln Arg Ala Leu Ser Thr Trp Lys
        165              170              175

caa atg ggg gag caa cgt gag cta cag gaa ggc acc tat gtg atg gtg      694
Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr Val Met Val
180              185              190              195

gca ggc ccc agc ttt gag act gtg gca gaa tgt cgt gtg ctg cag aag      742
Ala Gly Pro Ser Phe Glu Thr Val Ala Glu Cys Arg Val Leu Gln Lys
                200              205              210

ctg gga gca gac gct gtt ggc atg agt aca gta cca gaa gtt atc gtt      790
Leu Gly Ala Asp Ala Val Gly Met Ser Thr Val Pro Glu Val Ile Val
            215              220              225

gca cgg cac tgt gga ctt cga gtc ttt ggc ttc tca ctc atc act aac      838
Ala Arg His Cys Gly Leu Arg Val Phe Gly Phe Ser Leu Ile Thr Asn
        230              235              240

aag gtc atc atg gat tat gaa agc ctg gag aag gcc aac cat gaa gaa      886
Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn His Glu Glu
        245              250              255

gtc tta gca gct ggc aaa caa gct gca cag aaa ttg gaa cag ttt gtc      934
Val Leu Ala Ala Gly Lys Gln Ala Ala Gln Lys Leu Glu Gln Phe Val
260              265              270              275

tcc att ctt atg gcc agc att cca ctc cct gac aaa gcc agt tga         979
Ser Ile Leu Met Ala Ser Ile Pro Leu Pro Asp Lys Ala Ser
                280              285

cctgccttgg agtcgtctgg catctcccac acaagaccca agtagctgct accttctttg    1039

gccccttgct ggagtcatgt gcctctgtcc ttaggttgta gcagaaagga aaagattcct    1099

gtccttcacc tttcccactt tcttctacca gacccttctg gtgccagatc ctcttctcaa    1159
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agctgggatt acaggtgtga gcatagtgag accttggcgc tacaaaataa agctgttctc   1219

attcctgttc tttcttacac aagagctgga gcccgtgccc taccacacat ctgtggagat   1279

gcccaggatt tgactcgggc cttagaactt tgcatagcag ctgctactag ctctttgaga   1339

taatacattc cgaggggctc agttctgcct tatctaaatc accagagacc aaacaaggac   1399

taatccaata cctcttgga   1418

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<212> PRT
<213> Homo sapiens

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Leu Leu Ser His Thr Lys His Arg Pro Gln Val Ala Ile Ile Cys Gly
            20   25   30

Ser Gly Leu Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe
            35   40   45

Asp Tyr Ser Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His
    50   55   60

Ala Gly Arg Leu Val Phe Gly Phe Leu Asn Gly Arg Ala Cys Val Met
65   70   75   80

Met Gln Gly Arg Phe His Met Tyr Glu Gly Tyr Pro Leu Trp Lys Val
                85   90   95

Thr Phe Pro Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val
                100   105   110

Val Thr Asn Ala Ala Gly Gly Leu Asn Pro Lys Phe Glu Val Gly Asp
                115   120   125

Ile Met Leu Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln
        130   135   140

Asn Pro Leu Arg Gly Pro Asn Asp Glu Arg Phe Gly Asp Arg Phe Pro
145   150   155   160

Ala Met Ser Asp Ala Tyr Asp Arg Thr Met Arg Gln Arg Ala Leu Ser
            165   170   175

Thr Trp Lys Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr
            180   185   190

Val Met Val Ala Gly Pro Ser Phe Glu Thr Val Ala Glu Cys Arg Val
        195   200   205

Leu Gln Lys Leu Gly Ala Asp Ala Val Gly Met Ser Thr Val Pro Glu
    210   215   220

Val Ile Val Ala Arg His Cys Gly Leu Arg Val Phe Gly Phe Ser Leu
225   230   235   240

Ile Thr Asn Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn
            245   250   255

His Glu Glu Val Leu Ala Ala Gly Lys Gln Ala Ala Gln Lys Leu Glu
        260   265   270

Gln Phe Val Ser Ile Leu Met Ala Ser Ile Pro Leu Pro Asp Lys Ala
        275   280   285

Ser

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<212> DNA
<213> Homo sapiens

<220>
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<222> (11)..(1642)

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            Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala
            1   5   10

att aaa tac aga cct gaa aat act cca gag cct gtc agt aca agt gtg   97
Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val
    15   20   25

agc cat tat gga gca gaa ccc act aca gtg tca cca tgt ccg tca tct   145

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Ser His Tyr Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser
30              35               40              45


tca gca aag gga aca gca gtt aat ttc agc agt ctt tcc atg aca cca      193
Ser Ala Lys Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro
                50              55              60


ttt gga gga tcc tca ggg gta acg cct ttt gga ggt gca tct tcc tca      241
Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser
                65              70              75


ttt tca gtg gtg cca agt tca tat cct gct ggt tta aca ggt ggt gtt      289
Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val
            80              85              90


act ata ttt gtg gcc tta tat gat tat gaa gct aga act aca gaa gac      337
Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp
        95              100             105


ctt tca ttt aag aag ggt gaa aga ttt caa ata att aac aat acg gaa      385
Leu Ser Phe Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu
110             115             120             125


gga gat tgg tgg gaa gca aga tca atc gct aca gga aag aat ggt tat      433
Gly Asp Trp Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr
                130             135             140


atc ccg agc aat tat gta gcg cct gca gat tcc att cag gca gaa gaa      481
Ile Pro Ser Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu
                145             150             155


tgg tat ttt ggc aaa atg ggg aga aaa gat gct gaa aga tta ctt ttg      529
Trp Tyr Phe Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu
                160             165             170


aat cct gga aat caa cga ggt att ttc tta gta aga gag agt gaa aca      577
Asn Pro Gly Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr
            175             180             185


act aaa ggt gct tat tcc ctt tct att cgt gat tgg gat gag ata agg      625
Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg
190             195             200             205


ggt gac aat gtg aaa cac tac aaa att agg aaa ctt gac aat ggt gga      673
Gly Asp Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly
                210             215             220


tac tat atc aca acc aga gca caa ttt gat act ctg cag aaa ttg gtg      721
Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val
            225             230             235


aaa cac tac aca gaa cat gct gat ggt tta tgc cac aag ttg aca act      769
Lys His Tyr Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr
            240             245             250


gtg tgt cca act gtg aaa cct cag act caa ggt cta gca aaa gat gct      817
Val Cys Pro Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala
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        255                     260                     265

tgg gaa atc cct cga gaa tct ttg cga cta gag gtt aaa cta gga caa      865
Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln
270                 275                 280                 285

gga tgt ttc ggc gaa gtg tgg atg gga aca tgg aat gga acc acg aaa      913
Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys
                    290                 295                 300

gta gca atc aaa aca cta aaa cca ggt aca atg atg cca gaa gct ttc      961
Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe
                305                 310                 315

ctt caa gaa gct cag ata atg aaa aaa tta aga cat gat aaa ctt gtt     1009
Leu Gln Glu Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val
            320                 325                 330

cca cta tat gct gtt gtt tct gaa gaa cca att tac att gtc act gaa     1057
Pro Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu
            335                 340                 345

ttt atg tca aaa gga agc tta tta gat ttc ctt aag gaa gga gat gga     1105
Phe Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly
350                 355                 360                 365

aag tat ttg aag ctt cca cag ctg gtt gat atg gct gct cag att gct     1153
Lys Tyr Leu Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala
                370                 375                 380

gat ggt atg gca tat att gaa aga atg aac tat att cac cga gat ctt     1201
Asp Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu
            385                 390                 395

cgg gct gct aat att ctt gta gga gaa aat ctt gtg tgc aaa ata gca     1249
Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala
            400                 405                 410

gac ttt ggt tta gca agg tta att gaa gac aat gaa tac aca gca aga     1297
Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg
    415                 420                 425

caa ggt gca aaa ttt cca atc aaa tgg aca gct cct gaa gct gca ctg     1345
Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu
430                 435                 440                 445

tat ggt cgg ttt aca ata aag tct gat gtc tgg tca ttt gga att ctg     1393
Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
                450                 455                 460

caa aca gaa cta gta aca aag ggc cga gtg cca tat cca ggt atg gtg     1441
Gln Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val
            465                 470                 475

aac cgt gaa gta cta gaa caa gtg gag cga gga tac agg atg ccg tgc     1489
Asn Arg Glu Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys
            480                 485                 490
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cct cag ggc tgt cca gaa tcc ctc cat gaa ttg atg aat ctg tgt tgg      1537
Pro Gln Gly Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp
    495                 500                 505

aag aag gac cct gat gaa aga cca aca ttt gaa tat att cag tcc ttc      1585
Lys Lys Asp Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe
510                 515                 520                 525

ttg gaa gac tac ttc act gct aca gag cca cag tac cag cca gga gaa      1633
Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu
                530                 535                 540

aat tta taa ttcaagtagc ctatttttata tgcacaaatc tgccaaaata           1682
Asn Leu


taaagaactt gtgtagattt tctacaggaa tcaaaagaag aaaatcttct ttactctgca    1742

tgtttttaat ggtaaactgg aatcccagat atggttgcac aaaaccactt ttttttcccc    1802

aagtattaaa ctctaatgta ccaatgatga atttatcagc gtatttcagg gtccaaacaa    1862

aatagagcta agatactgat gacagtgtgg gtgacagcat ggtaatgaag gacagtgagg    1922

ctcctgctta tttataaatc atttcctttc ttttttttccc caaagtcaga attgctcaaa   1982

gaaaattatt tattgttaca gataaaactt gagagataaa aagctatacc ataataaaat    2042

ctaaaattaa ggaatatcat gggaccaaat aattccattc cagttttta aagtttcttg     2102

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cctcacttag ctatattctg agactttgaa gagttataaa gtataactat aaaactaatt    2822

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ggctggagtg cagtggcgcg atctcggctc actgcaagct ctgcctccca ggttcacacc    3062

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tttagaatac attaaatggt tgatttgggg aggaaaactt attctgaata ttaacggtgg    3362

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<212> PRT
<213> Homo sapiens

<400> 9

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Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
            20              25              30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
        35              40              45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
    50              55              60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
65              70              75              80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
            85              90              95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
        100             105             110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
    115             120             125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
    130             135             140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
145             150             155             160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
            165             170             175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
            180             185             190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
        195             200             205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
    210             215             220
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Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
225             230             235             240


Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
                245             250             255


Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
            260             265             270


Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
        275             280             285


Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
    290             295             300


Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
305             310             315             320


Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
            325             330             335


Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
            340             345             350


Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
        355             360             365


Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
    370             375             380


Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
385             390             395             400


Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
            405             410             415


Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
        420             425             430


Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
        435             440             445


Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
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Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
465   470   475   480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
                485   490   495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
            500   505   510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
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